

C. Saoud

Page 1 of 5

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

3 <110> APPLICANT: Walker, Ameae M.
5 <120> TITLE OF INVENTION: PROLACTIN ANTAGONISTS AND USES THEREOF
7 <130> FILE REFERENCE: Walker_2500_097US2
9 <140> CURRENT APPLICATION NUMBER: 09/065,330B
10 <141> CURRENT FILING DATE: 1998-04-23
12 <150> PRIOR APPLICATION NUMBER: PCT/US97/01435
13 <151> PRIOR FILING DATE: 1997-01-30
15 <150> PRIOR APPLICATION NUMBER: 08/594,809
16 <151> PRIOR FILING DATE: 1996-01-31
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 832
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: mutation
29 <222> LOCATION: (622)..(624)
30 <223> OTHER INFORMATION: This is the codon for the substituted amino acids
31 of the mutated sequence.
33 <400> SEQUENCE: 1
34 aacatgaaca tcaaaggatc gccatggaaa gggcccttc tgcgtgtgt ggtgtcaa 60
35 ctgtgtgtt gccagacgt ggccccctt cccatgttc cccgcggggc tgcccgtgc 120
36 caggtagcc ttccgaccc tttgacccgc gccgtgttc tgcgttacta catccataac 180
37 ctcccttcag aatgttcag cgaatccat aaacggata cccatggccg ggggttcatt 240
38 accaaggcca tcaacagctg ccacacttct tcccttgcctt cccccaaga caaggagcaa 300
39 gcccaacaga tgaatcaaaa agactttctg agcctgtatg tcaagatatt ggcatactgg 360
40 aatgagccct tgcgtatcatct ggtcacggaa gtacgtgtt tgcagaaga cccggaggct 420
41 atccatccaa aagctgtaga gattgaggag caaaccacaa ggcttctaga gggcatggag 480
42 ctgtatgtca gccagggttca tccgtggaaacc aaagaaaaatg agatctaccc tgcgtggtcg 540
43 ggacttccat ccctgcagat ggctgtatgaa gatgttcgc tttctgttataaccctg 600
44 ctccactgct tacgcaggaa tmnncataaa atcgacaatt atctcaagct cctgaagtgc 660
45 cgaatccatc acaacaacaa ctgtcaagcc cacatccatt tcatctatctt ctgagaagg 720
46 ctttaatgtat ccgttccatt gcaagcttct tttatgttgc tctcttttgc atccatgtt 780
47 ggggtgtaaaca ggttcccttataaa aactgactc gtttagagaca tc 832
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 228
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <220> FEATURE:
57 <221> NAME/KEY: VARIANT
58 <222> LOCATION: (208)
59 <223> OTHER INFORMATION: Site mutated codon where the normal codon coding
60 for serine is modified preferably to encode for
61 aspartate or glutamate, most preferably aspartate.
63 <400> SEQUENCE: 2
64 Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu

Does Not Comply
Corrected Diskette Needed

pp 1-3

? a codon consists of three bases

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```

65 1 5 10 15
67 Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
68 20 25 30
70 Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
71 35 40 45
73 Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
74 50 55 60
76 Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
77 65 70 75 80
79 Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
80 85 90 95
82 Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
83 100 105 110
85 Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
86 115 120 125
88 Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
89 130 135 140
91 Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
92 145 150 155 160
94 Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
95 165 170 175
97 Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
98 180 185 190
W--> 101 Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
102 195 200 205
104 His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
105 210 215 220
107 Asn Asn Asn Cys
108 225
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 23
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
119 is a primer.
121 <400> SEQUENCE: 3
122 gcaggatga ccacaagggtt gac
125 <210> SEQ ID NO: 4
126 <211> LENGTH: 24
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
132 is a primer.
134 <220> FEATURE:
135 <221> NAME/KEY: variation
136 <222> LOCATION: (12)
137 <223> OTHER INFORMATION: This is a codon that can be replaced for nucleic

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A codon consists of three bases - location 12 "n" is only one

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138 acid substitutes.
140 <400> SEQUENCE: 4
W--> 141 cgcaaggat gmacacaagg ttga 24
144 <210> SEQ ID NO: 5
145 <211> LENGTH: 22
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
153 is a primer.
155 <220> FEATURE:
156 <221> NAME/KEY: variation
157 <222> LOCATION: (12)
158 <223> OTHER INFORMATION: This is a *codon* that can be replaced for nucleic
159 acid substitutes.
161 <400> SEQUENCE: 5
W--> 162 acgcaggat gkataaaat cg 22
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 26
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
172 is a primer.
174 <400> SEQUENCE: 6
175 cgtggccccc atatgttgc catctg 26
W--> 176

hand error
delete at end of file

VERIFICATION SUMMARY
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Input Set : A:\Sequence.Lst.txt
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L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6